

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/802,472

DATE: 07/09/2001

TIME: 12:44:34

Input Set : A:\EINAT4-1C.txt

Output Set: N:\CRF3\07092001\I802472.raw

Does Not Comply  
Corrected Diskette Needed

pg 3, 5-6

3 &lt;110&gt; APPLICANT: EINAT, Paz

4 SKALITER, Rami

5 FEINSTEIN, Elena

7 &lt;120&gt; TITLE OF INVENTION: SEQUENCES CHARACTERISTIC OF HYPOXIA-REGULATED GENE

## TRANSCRIPTION

9 &lt;130&gt; FILE REFERENCE: EINAT=4.1C

11 &lt;140&gt; CURRENT APPLICATION NUMBER: US/09/802,472

11 &lt;141&gt; CURRENT FILING DATE: 2001-03-09

11 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/383,096

12 &lt;151&gt; PRIOR FILING DATE: 1999-08-27

14 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/138,109

15 &lt;151&gt; PRIOR FILING DATE: 1998-08-21

17 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/098,158

18 &lt;151&gt; PRIOR FILING DATE: 1998-08-27

20 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/132,684

21 &lt;151&gt; PRIOR FILING DATE: 1999-05-05

23 &lt;160&gt; NUMBER OF SEQ ID NOS: 21

25 &lt;170&gt; SOFTWARE: PatentIn version 3.0

27 &lt;210&gt; SEQ ID NO: 1

28 &lt;211&gt; LENGTH: 1655

29 &lt;212&gt; TYPE: DNA

30 &lt;213&gt; ORGANISM: Homo sapiens

32 &lt;220&gt; FEATURE:

33 &lt;221&gt; NAME/KEY: CDS

34 &lt;222&gt; LOCATION: (265)..(1575)

36 &lt;220&gt; FEATURE:

37 &lt;221&gt; NAME/KEY: misc feature

38 &lt;223&gt; OTHER INFORMATION: "n" at every occurrence is unknown

41 &lt;400&gt; SEQUENCE: 1

42 gcacnaggtg tgtggcagca anagccgccg gttcgggacc nccgcantcg ggggtggcaac 60  
 44 ggcgcaggag gggctgcggg gagggagtg tgagcgcagg cggcaggggt ctgggaaaga 120  
 46 cgaagtcgct atttgctgtc tgagcgcgct cgcagctcct ggaagtgttg ccgcctctcg 180  
 48 gtttcgctct cgctcgctgc gctcctagaa ggggcggcgg cctccaggac tgaccagggc 240  
 50 caagtggcgc tcggcgggca ctac atg gcg gag ggt gaa ggg tac ttc gcc 291  
 51 Met Ala Glu Gly Glu Gly Tyr Phe Ala  
 52 1 5  
 54 atg tct gag gac gag ctg gcc tgc agc ccc tac atc ccc cta ggc ggc 339  
 55 Met Ser Glu Asp Glu Leu Ala Cys Ser Pro Tyr Ile Pro Leu Gly Gly  
 56 10 15 20 25  
 58 gac ttc ggc ggc ggc gac ttc ggc ggc ggc gac ttc ggc ggt ggc ggc 387  
 59 Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Asp Phe Gly Gly Gly Gly  
 60 30 35 40  
 62 agc ttc ggt ggg cat tgc ttg gac tat tgc gaa agc cct acg gcg cac 435  
 63 Ser Phe Gly Gly His Cys Leu Asp Tyr Cys Glu Ser Pro Thr Ala His  
 64 45 50 55  
 66 tgc aat gtg ctg aac tgg gag caa gtg cag cgg ctg gac ggc atc ctg 483  
 67 Cys Asn Val Leu Asn Trp Glu Gln Val Gln Arg Leu Asp Gly Ile Leu  
 68 60 65 70

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70	agc	gag	acc	att	ccg	att	cac	ggg	cgc	ggc	aac	ttc	ccc	acg	ctc	gag	531
71	Ser	Glu	Thr	Ile	Pro	Ile	His	Gly	Arg	Gly	Asn	Phe	Pro	Thr	Leu	Glu	
72		75					80				85						
74	ctg	cag	cgc	agc	ctg	atc	gtg	aag	gtg	gtg	cgg	cgg	cgc	ctg	gcc	gag	579
75	Leu	Gln	Pro	Ser	Leu	Ile	Val	Lys	Val	Val	Arg	Arg	Arg	Leu	Ala	Glu	
76	90					95					100					105	
78	aag	cgc	att	ggc	gtc	cgc	gac	gtg	cgc	ctc	aac	ggc	tcg	gca	gcc	agc	627
79	Lys	Arg	Ile	Gly	Val	Arg	Asp	Val	Arg	Leu	Asn	Gly	Ser	Ala	Ala	Ser	
80				110						115					120		
82	cat	gtc	ctg	cac	cag	gac	agc	ggc	ctg	ggc	tac	aag	gac	ctg	gac	ctc	675
83	His	Val	Leu	His	Gln	Asp	Ser	Gly	Leu	Gly	Tyr	Lys	Asp	Leu	Asp	Leu	
84				125					130					135			
86	atc	ttc	tgc	gcc	gac	ctg	cgc	ggg	gaa	ggg	gag	ttt	cag	act	gtg	aag	723
87	Ile	Phe	Cys	Ala	Asp	Leu	Arg	Gly	Glu	Gly	Glu	Phe	Gln	Thr	Val	Lys	
88			140					145				150					
90	gac	gtc	gtg	ctg	gac	tgc	ctg	ttg	gac	ttc	tta	ccc	gag	ggg	gtg	aac	771
91	Asp	Val	Val	Leu	Asp	Cys	Leu	Leu	Asp	Phe	Leu	Pro	Glu	Gly	Val	Asn	
92		155				160					165						
94	aaa	gag	aag	atc	aca	cca	ctc	acg	ctc	aag	gaa	gct	tat	gtg	cag	aaa	819
95	Lys	Glu	Lys	Ile	Thr	Pro	Leu	Thr	Leu	Lys	Glu	Ala	Tyr	Val	Gln	Lys	
96	170				175					180					185		
98	atg	ggt	aaa	gtg	tgc	aat	gac	tct	gac	cga	tgg	agt	ctt	ata	tcc	ctg	867
99	Met	Val	Lys	Val	Cys	Asn	Asp	Ser	Asp	Arg	Trp	Ser	Leu	Ile	Ser	Leu	
100				190					195				200				
102	tca	aac	aac	agt	ggc	aaa	aat	gtg	gaa	ctg	aaa	ttt	gtg	gat	tcc	ctc	915
103	Ser	Asn	Asn	Ser	Gly	Lys	Asn	Val	Glu	Leu	Lys	Phe	Val	Asp	Ser	Leu	
104			205					210				215					
106	cgg	agg	cag	ttt	gaa	ttc	agt	gta	gat	tct	ttt	caa	atc	aaa	tta	gac	963
107	Arg	Arg	Gln	Phe	Glu	Phe	Ser	Val	Asp	Ser	Phe	Gln	Ile	Lys	Leu	Asp	
108			220				225				230						
110	tct	ctt	ctg	ctc	ttt	tat	gaa	tgt	tca	gag	aac	cca	atg	act	gag	aca	1011
111	Ser	Leu	Leu	Leu	Phe	Tyr	Glu	Cys	Ser	Glu	Asn	Pro	Met	Thr	Glu	Thr	
112		235				240					245						
114	ttt	cac	ccc	aca	ata	atc	ggg	gag	agc	gtc	tat	ggc	gat	ttc	cag	gaa	1059
115	Phe	His	Pro	Thr	Ile	Ile	Gly	Glu	Ser	Val	Tyr	Gly	Asp	Phe	Gln	Glu	
116	250				255					260				265			
118	gcc	ttt	gat	cac	ctt	tgt	aac	aag	atc	att	gcc	acc	agg	aac	cca	gag	1107
119	Ala	Phe	Asp	His	Leu	Cys	Asn	Lys	Ile	Ile	Ala	Thr	Arg	Asn	Pro	Glu	
120				270					275					280			
122	gaa	atc	cga	ggg	gga	ggc	ctg	ctt	aag	tac	tgc	aac	ctc	ttg	gtg	agg	1155
123	Glu	Ile	Arg	Gly	Gly	Gly	Leu	Leu	Lys	Tyr	Cys	Asn	Leu	Leu	Val	Arg	
124			285				290					295					
126	ggc	ttt	agg	ccc	gcc	tct	gat	gaa	atc	aag	acc	ctt	caa	agg	tat	atg	1203
127	Gly	Phe	Arg	Pro	Ala	Ser	Asp	Glu	Ile	Lys	Thr	Leu	Gln	Arg	Tyr	Met	
128			300				305					310					
130	tgt	tcc	agg	ttt	ttc	atc	gac	ttc	tca	gac	att	gga	gag	cag	cag	aga	1251
131	Cys	Ser	Arg	Phe	Phe	Ile	Asp	Phe	Ser	Asp	Ile	Gly	Glu	Gln	Gln	Arg	
132		315				320					325						
134	aaa	ctg	gag	tcc	tat	ttg	cag	aac	ctc	ttt	gtg	gga	ttg	gaa	gcc	cgc	1299

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```

135 Lys Leu Glu Ser Tyr Leu Gln Asn Leu Phe Val Gly Leu Glu Ala Arg
136 330 335 340 345
138 aag tat gag tat ctc atg acc ctt cat gga gtg gta aat gag agc tca 1347
139 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Ser
140 350 355 360
142 gtg tgc ctg atg gga cat gaa aga aga cag act tta aac ctt atc acc 1395
143 Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr
144 365 370 375
146 atg ctg gct atc cgg gtg tta gct gac caa aat gtc att cct aat gtg 1443
147 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val
148 380 385 390
150 gct aat gtc act tgc tat tac cag cca gcc ccc tat gta gca gat gcc 1491
151 Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
152 395 400 405
154 aac ttt agc aat tac tac att gca cag gtt cag cca gta ttc acg tgc 1539
155 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys
156 410 415 420 425
158 cag caa cag acc tac tcc act tgg cta ccc tgc aat taagaatcat 1585
159 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn
160 430 435
162 ttaaaaatgt cctgtgggga agccatttca gacaagacag gagagaaaaa aaaaaaaaaa 1645
164 aaaaaaaaaa 1655
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 437
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: misc feature
174 <223> OTHER INFORMATION: "n" at every occurrence is unknown
176 <400> SEQUENCE: 2
178 Met Ala Glu Gly Glu Gly Tyr Phe Ala Met Ser Glu Asp Glu Leu Ala
179 1 5 10 15
182 Cys Ser Pro Tyr Ile Pro Leu Gly Gly Asp Phe Gly Gly Gly Asp Phe
183 20 25 30
186 Gly Gly Gly Asp Phe Gly Gly Gly Gly Ser Phe Gly Gly His Cys Leu
187 35 40 45
190 Asp Tyr Cys Glu Ser Pro Thr Ala His Cys Asn Val Leu Asn Trp Glu
191 50 55 60
194 Gln Val Gln Arg Leu Asp Gly Ile Leu Ser Glu Thr Ile Pro Ile His
195 65 70 75 80
198 Gly Arg Gly Asn Phe Pro Thr Leu Glu Leu Gln Pro Ser Leu Ile Val
199 85 90 95
202 Lys Val Val Arg Arg Arg Leu Ala Glu Lys Arg Ile Gly Val Arg Asp
203 100 105 110
206 Val Arg Leu Asn Gly Ser Ala Ala Ser His Val Leu His Gln Asp Ser
207 115 120 125
210 Gly Leu Gly Tyr Lys Asp Leu Asp Leu Ile Phe Cys Ala Asp Leu Arg
211 130 135 140
214 Gly Glu Gly Glu Phe Gln Thr Val Lys Asp Val Val Leu Asp Cys Leu

```

*delete-amino acid sequences  
would contain  
Xaa, not "n"*

*Besides, no  
Xaa is  
shown in  
the sequence*

*"n" is only  
used in  
nucleotide  
sequence*

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```

215 145          150          155          160
218 Leu Asp Phe Leu Pro Glu Gly Val Asn Lys Glu Lys Ile Thr Pro Leu
219          165          170          175
222 Thr Leu Lys Glu Ala Tyr Val Gln Lys Met Val Lys Val Cys Asn Asp
223          180          185          190
226 Ser Asp Arg Trp Ser Leu Ile Ser Leu Ser Asn Asn Ser Gly Lys Asn
227          195          200          205
230 Val Glu Leu Lys Phe Val Asp Ser Leu Arg Arg Gln Phe Glu Phe Ser
231          210          215          220
234 Val Asp Ser Phe Gln Ile Lys Leu Asp Ser Leu Leu Leu Phe Tyr Glu
235 225          230          235          240
238 Cys Ser Glu Asn Pro Met Thr Glu Thr Phe His Pro Thr Ile Ile Gly
239          245          250          255
242 Glu Ser Val Tyr Gly Asp Phe Gln Glu Ala Phe Asp His Leu Cys Asn
243          260          265          270
246 Lys Ile Ile Ala Thr Arg Asn Pro Glu Glu Ile Arg Gly Gly Gly Leu
247          275          280          285
250 Leu Lys Tyr Cys Asn Leu Leu Val Arg Gly Phe Arg Pro Ala Ser Asp
251          290          295          300
254 Glu Ile Lys Thr Leu Gln Arg Tyr Met Cys Ser Arg Phe Phe Ile Asp
255 305          310          315          320
258 Phe Ser Asp Ile Gly Glu Gln Gln Arg Lys Leu Glu Ser Tyr Leu Gln
259          325          330          335
262 Asn Leu Phe Val Gly Leu Glu Ala Arg Lys Tyr Glu Tyr Leu Met Thr
263          340          345          350
266 Leu His Gly Val Val Asn Glu Ser Ser Val Cys Leu Met Gly His Glu
267          355          360          365
270 Arg Arg Gln Thr Leu Asn Leu Ile Thr Met Leu Ala Ile Arg Val Leu
271          370          375          380
274 Ala Asp Gln Asn Val Ile Pro Asn Val Ala Asn Val Thr Cys Tyr Tyr
275 385          390          395          400
278 Gln Pro Ala Pro Tyr Val Ala Asp Ala Asn Phe Ser Asn Tyr Tyr Ile
279          405          410          415
282 Ala Gln Val Gln Pro Val Phe Thr Cys Gln Gln Gln Thr Tyr Ser Thr
283          420          425          430
286 Trp Leu Pro Cys Asn
287          435
290 <210> SEQ ID NO: 3
291 <211> LENGTH: 3454
292 <212> TYPE: DNA
293 <213> ORGANISM: Homo sapiens
295 <220> FEATURE:
296 <221> NAME/KEY: CDS
297 <222> LOCATION: (323)..(1762)
299 <220> FEATURE:
300 <221> NAME/KEY: misc_feature
301 <223> OTHER INFORMATION: "n" at every occurrence is unknown
304 <400> SEQUENCE: 3
305 ctccgcggcg gggatgctga ggagcgctgg gtccgggagc agccctggcc cctgcggact

```

60

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```

307 tccgaggccg tgaaaacccc tgcgctgcgg cccttcccag gcccccgagg ccgttcgccc 120
309 ttcccgaagc ccgactgggg gaagagtcca gcaccaaagc ggccgttctc ggattccgga 180
311 gcgttctgga gccccgagag acgccccggg gttctagaag ctccccggcg gcgcccagtc 240
313 ccggcttcat tcgggcgtcc ctccgaaacc cactcgggtg cacgggtcgt cggcgagccc 300
315 cgaccgggtc ctggcgcgca cc atg atc gtg gcg gac tcc gag tgc cgc gca 352
316                               Met Ile Val Ala Asp Ser Glu Cys Arg Ala
317                               1               5               10
319 gag ctc aag gac tac ctg cgg ttc gcc ccg ggc ggc gtc ggc gac tcg 400
320 Glu Leu Lys Asp Tyr Leu Arg Phe Ala Pro Gly Gly Val Gly Asp Ser
321                               15               20               25
323 ggc ccc gga gag gag cag agg gag agc cgg gct cgg cga ggc cct cga 448
324 Gly Pro Gly Glu Glu Gln Arg Glu Ser Arg Ala Arg Arg Gly Pro Arg
325                               30               35               40
327 ggg ccc agc gcc ttc atc ccc gtg gag gag gtc ctt cgg gag ggg gct 496
328 Gly Pro Ser Ala Phe Ile Pro Val Glu Glu Val Leu Arg Glu Gly Ala
329                               45               50               55
331 gag agc ctc gag cag cac ctg ggg ctg gag gca ctg atg tcc tct ggg 544
332 Glu Ser Leu Glu Gln His Leu Gly Leu Glu Ala Leu Met Ser Ser Gly
333                               60               65               70
335 cga gta gac aac ctg gca gtg gtg atg ggc ctg cac cct gac tac ttt 592
336 Arg Val Asp Asn Leu Ala Val Val Met Gly Leu His Pro Asp Tyr Phe
337 75                               80               85               90
339 acc agc ttc tgg cnc ctg cac tac ctg ctg ctg cac acg gat ggt ccc 640
340 Thr Ser Phe Trp Xaa Leu His Tyr Leu Leu Leu His Thr Asp Gly Pro
341                               95               100              105
343 ttg gcc agc tcc tgg cgc cac tac att gcc atc atg gct gcc gcc cgc 688
344 Leu Ala Ser Ser Trp Arg His Tyr Ile Ala Ile Met Ala Ala Ala Arg
345                               110              115              120
347 cat cag tgt tct tac ctg gta ggc tcc cac atg gcc gag ttt ctg cag 736
348 His Gln Cys Ser Tyr Leu Val Gly Ser His Met Ala Glu Phe Leu Gln
349                               125              130              135
351 act ggt ggt gac cct gag tgg ctg ctg ggc ctc cac cgg gcc ccc gag 784
352 Thr Gly Gly Asp Pro Glu Trp Leu Leu Gly Leu His Arg Ala Pro Glu
353                               140              145              150
355 aag ctg cgc aaa ctc agc gag atc aac aag ttg ctg gcg cat cgg cca 832
356 Lys Leu Arg Lys Leu Ser Glu Ile Asn Lys Leu Leu Ala His Arg Pro
357 155                               160              165              170
359 tgg ctc atc acc aag gaa cac atc cag gcc ttg ctg aag acc ggc gag 880
360 Trp Leu Ile Thr Lys Glu His Ile Gln Ala Leu Leu Lys Thr Gly Glu
361                               175              180              185
363 cac act tgg tcc ctg gcc gag ctc att cag gct ctg gtc ctg ctc acc 928
364 His Thr Trp Ser Leu Ala Glu Leu Ile Gln Ala Leu Val Leu Leu Thr
365                               190              195              200
367 cac tgc cac tcg ctc tcc tcc ttc gtg ttt ggc tgt ggc atc ctc cct 976
368 His Cys His Ser Leu Ser Ser Phe Val Phe Gly Cys Gly Ile Leu Pro
369                               205              210              215
371 gag ggg gat gca gat ggc agc cct gcc ccc cag gca cct aca ccc cct 1024
372 Glu Gly Asp Ala Asp Gly Ser Pro Ala Pro Gln Ala Pro Thr Pro Pro
373                               220              225              230

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

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<210> 4  
<211> 480  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc feature  
<223> "n" at every occurrence is unknown

*This is an amino acid sequence;*

<400> 4

*Xaa is shown below*

Met Ile Val Ala Asp Ser Glu Cys Arg Ala Glu Leu Lys Asp Tyr Leu  
1 5 10 15

Arg Phe Ala Pro Gly Gly Val Gly Asp Ser Gly Pro Gly Glu Glu Gln  
20 25 30

Arg Glu Ser Arg Ala Arg Arg Gly Pro Arg Gly Pro Ser Ala Phe Ile  
35 40 45

Pro Val Glu Glu Val Leu Arg Glu Gly Ala Glu Ser Leu Glu Gln His  
50 55 60

Leu Gly Leu Glu Ala Leu Met Ser Ser Gly Arg Val Asp Asn Leu Ala  
65 70 75 80

Val Val Met Gly Leu His Pro Asp Tyr Phe Thr Ser Phe Trp Xaa Leu  
85 90 95

His Tyr Leu Leu Leu His Thr Asp Gly Pro Leu Ala Ser Ser Trp Arg  
100 105 110

His Tyr Ile Ala Ile Met Ala Ala Ala Arg His Gln Cys Ser Tyr Leu  
115 120 125

Val Gly Ser His Met Ala Glu Phe Leu Gln Thr Gly Gly Asp Pro Glu  
130 135 140

Trp Leu Leu Gly Leu His Arg Ala Pro Glu Lys Leu Arg Lys Leu Ser  
145 150 155 160

Glu Ile Asn Lys Leu Leu Ala His Arg Pro Trp Leu Ile Thr Lys Glu  
165 170 175

His Ile Gln Ala Leu Leu Lys Thr Gly Glu His Thr Trp Ser Leu Ala  
180 185 190

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

*(only the error portion of seq. 4 shown)*

**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:527 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:783 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:785 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:821 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:823 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:825 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:861 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:2527 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:2539 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
L:2539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20